EXHIBIT 1

Alignment of SEQ ID NO:1 (10/609,150) and SEQ ID NO:5 (Schweighoffer)

Score = 404 bits (210),   Expect = 4e-109
 Identities = 612/813 (75%), Gaps = 0/813 [Note- alignment across the entire Schweighoffer sequence gives an alignment of 612/865= 71% homology]

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SEQ5   52    CATAATATTACATTTCAGAGTTCACCTCCCACAGTTGAGTGGCATATAAGCAGACCTGGG  111
             ||||||||||| ||| | ||| |||||||| || |||| |||||||||| |||| ||| ||
SEQ1   2242  CATAATATTACCTTTGAAAGTCCACCTCCACCAATTGAATGGCATATCAGCAAACCAGGA  2301

Query  112   CACATAGAGACTTTTGACCTGCTCACCTTACACCCAATAGAAATTGCTCGACAACTCACT  171
             ||  | || || ||||| ||   ||| |   | ||||||||||||||| || || || ||
Sbjct  2302  CAGTTTGAAACATTTGATCTCATGACACTTGATCCAATAGAAATTGCACGTCAGCTGACA  2361

Query  172   TTACTTGATTCAGATCTATACCGAGCTGTACAGCCATCAGATTTAGTTGGAAGTGTGTGG  231
             | | || || ||||| |||  |  || || || || || || | ||| || |||||||||
Sbjct  2362  CTTTTGGAGTCTGATCTTTACAGGAAAGTTCAACCGTCTGAACTTGTAGGGAGTGTGTGG  2421

Query  232   ACAAAAGAAGACAAAGAAATTAACTCTCCTAATCTTCTGAAAATGATTCGACATACCACC  291
             || ||||||||| |||||||| || ||||| ||| |  | |||||||||||| ||||||||
Sbjct  2422  ACCAAAGAAGATAAAGAAATAAATTCTCCAAATTTATTAAAAATGATTCGCCATACCACA  2481

Query  292   AACCTCACTCTGTGGTTTGAGAAATGTATTGTAGAAACTGAAAATTTAGAAGAAAGAGTA  351
             || ||||| || |||||||| ||||| |||||| ||| ||| ||| | ||||||| | ||
Sbjct  2482  AATCTCACCCTCTGGTTTGAAAAATGCATTGTGGAAGCAGAAAATTTTGAAGAACGGGTG  2541

Query  352   GCTGTGGTGAGTCGAATTATTGAGATTCTACAAGTCTTTCAAGAGTTGAACAACTTTAAT  411
             || ||   | ||| |||||||| || ||||| ||||| |||||||||| ||||| || || |||
Sbjct  2542  GCAGTACTAAGTAGAATTATAGAAATTCTGCAAGTTTTTCAAGATTTGAATAATTTCAAT  2601

Query  412   GGGGTCCTTGAGGTTGTCAGTGCTATGAATTCCTCACCTGTTTACAGACTAGACCACACA  471
             || ||  | ||| | |||||||||  | |||||     | || |||||||||||||| ||
Sbjct  2602  GGCGTATTGGAGATAGTCAGTGCAGTAAATTCAGTGTCAGTATACAGACTAGACCATACC  2661

Query  472   TTTGAGCAAATACCAAGTCGCCAGAAGAAAATTTTAGAAGAAGCTCATGAATTGAGTGAA  531
             ||||||   | | |        | | | ||||||||| || ||||||    ||||| ||| ||
Sbjct  2662  TTTGAGGCACTGCAGGAAAGGAAAAGGAAAATTTTGGACGAAGCTGTGGAATTAAGTCAA  2721

Query  532   GATCACTATAAGAAATATTTGGCAAAACTCAGGTCTATTAATCCACCATGTGTGCCTTTC  591
             ||||||| ||| ||||| | | ||||||| | ||| || ||||||||| |||||||||||
Sbjct  2722  GATCACTTTAAAAAATACCTAGTAAAACTTAAGTCAATCAATCCACCTTGTGTGCCTTTT  2781

Query  592   TTTGGAATTTATCTACATAATATCTTGAAAACAGAAGAAGGCAACCCTGAGGTCCTAAAA  651
             |||||||| ||| || |   ||||| | |||| || || ||||||||| ||   ||| | ||||
Sbjct  2782  TTTGGAATATATTTAACAAATATTCTGAAGACCGAAGAAGGGAATAATGATTTTTTAAAA  2841

Query  652   AGACATGGAAAAGAGCTTATAAACTTTAGCAAAAGGAGGAAAGTAGCAGAAATAACAGGA  711
             ||| | | ||||||| | || || || || || || || ||||||||||||||| || |||
Sbjct  2842  AGAAAGGGAAAAGATTTAATCAATTTCAGTAAGAGGAGGAAAGTAGCTGAAATTACTGGA  2901

Query  712   GAGATCCAGCAGTACCAAAATCAGCCTTACTGTTTACGAGTAGAATCAGATATCAAAAGG  771
             || || ||||||| ||||| ||||||||||||||||| |||||| |||||| |||| | ||
Sbjct  2902  GAAATTCAGCAGTATCAGAATCAGCCTTACTGTTTACGGATAGAACCAGATATGAGGAGA  2961

Query  772   TTCTTTGAAAACTTGAATCCGATGGGAAATAGCATGGAGAGGGAATTTACAGATTATCTT  831
             ||||||||||| | ||| || ||||||||||| |       || | || |||||||||| |
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Sbjct  2962  TTCTTTGAAAACCTTAACCCCATGGGAAGTGCATCTGAAAAAGAGTTTACAGATTATTTG  3021


Query  832   TTCAACAAATCCCTAGAAATAGAACCACGAAAC  864
             ||||||||| || ||||||||| |||||| ||||||
Sbjct  3022  TTCAACAAGTCACTAGAAATTGAACCTCGAAAC  3054
```

Alignment of 10/609,150 SEQ ID NO:2 with SEQ ID NO:1:

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Score = 48.8 bits (25),  Expect = 2e-04
 Identities = 25/25 (100%), Gaps = 0/25 (0%)
 Strand=Plus/Minus

Query  1     GAGGGTGAGATTTGTGGTATGGCGA  25
             |||||||||||||||||||||||||
Sbjct  2493  GAGGGTGAGATTTGTGGTATGGCGA  2469
```

Alignment of 10/609,150 SEQ ID NO:3 with SEQ ID NO:1:

```
Score = 48.8 bits (25),  Expect = 2e-04
 Identities = 25/25 (100%), Gaps = 0/25 (0%)
 Strand=Plus/Minus

Query  1     TGAGGAAAGGTCTTCTGAACTCGCT  25
             |||||||||||||||||||||||||
Sbjct  239   TGAGGAAAGGTCTTCTGAACTCGCT  215
```